AMENDMENTS TO THE CLAIMS

The claims are not amended. A complete listing of the claims, including their current status, is set forth below.

1-25 (canceled)

26. (previously presented) A method for identifying an intracellular target molecule that binds to a transdominant intracellular bioactive peptide that alters the phenotype of a cell, said method comprising the steps:

a) introducing a molecular library comprising different nucleic acid sequences into a plurality of cells, wherein said nucleic acid sequences each comprise a sequence encoding:

i) a candidate randomized peptide of from 4 to 100 amino acids in length, wherein said nucleic acid sequences are expressed in said cells to produce a plurality of randomized peptides;

b) screening said plurality of cells to identify a cell that has an altered phenotype and thereby identify a randomized peptide that (i) alters the cell phenotype when expressed, and (ii) is transdominant and intracellular;

c) identifying an intracellular target molecule to which said transdominant randomized peptide binds.

27. (previously presented) A method according to claim 26 wherein said identifying comprises:

d) isolating a cell having an altered phenotype as the result of expression of said transdominant bioactive peptide;

e) isolating said transdominant bioactive peptide; and

f) binding said transdominant bioactive agent to an intracellular target present in said cell to identify said target.

28. (canceled)

29. (previously presented) A method for identifying an intracellular target molecule that binds to a transdominant intracellular bioactive peptide that alters the phenotype of a cell, said method comprising the steps:

a) introducing a molecular library comprising different nucleic acid sequences into a plurality of cells, wherein said nucleic acid sequences each comprise a sequence encoding:

i) a candidate transdominant intracellular bioactive peptide of from 4 to 100 amino acids in length, comprising a randomized portion; and ii) presentation structure that presents said randomized bioactive peptides in a conformationally restricted form wherein a first portion of said presentation structure is joined to the N-terminal end of said candidate transdominant intracellular bioactive peptide, and a second portion of said presentation structure is joined to the C-terminal end of said candidate transdominant intracellular bioactive peptide, and wherein said nucleic acid sequences are expressed in said cells to produce a plurality of randomized peptides;

b) screening said plurality of cells to identify a cell that has an altered phenotype and thereby identify a randomized peptide that (i) alters the-cell phenotype when expressed, and (ii) is transdominant and intracellular;

c) identifying an intracellular target molecule to which said transdominant randomized peptide binds.

30. (canceled)

31. (previously presented) A method according to claim 26 wherein said cells are mammalian cells.

32. (previously presented) A method according to claim 26 wherein said library comprises at least 10^4 different nucleic acids.

33. (previously presented) A method according to claim 26 wherein said library comprises at least 10^5 different nucleic acids.

34. (previously presented) A method according to claim 26 wherein said library comprises at least 10^6 different nucleic acids.

35. (previously presented) A method according to claim 26 wherein said library comprises at least 10^7 different nucleic acids.

36. (previously presented) A method according to claim 26 wherein said library comprises at least 10^8 different nucleic acids.

37. (previously presented) A method according to claim 26 wherein each of said candidate nucleic acids is linked to nucleic acid encoding at least one fusion partner.

38-50 (canceled)